



Fig. 10

human : GDVEKGKIFIMKCSQCHTVEGGKHKTGPNLHGLFGRK SEQ ID NO: 1  
bacterium : EGDAAAGEKVSKKCLACHTFDQGGANKVGNPNLFGVF SEQ ID NO: 2

LCS : GD(x3.3)G(x0.1)K(x0.2)K(x4.0)KC(x2.2)CHT(x3.3)GG(x2.2)K  
GD(x1.4)E(x0.2)K(x0.2)K(x0.4)KC(x2.2)CHT(x3.3)GG(x2.2)K

homology : 47%



Fig. 11

Rat : MSLAILRVIRLVRVFRIFKLSRHSKGLQILGRTLKASMRELGLLFFIGVV

SEQ ID No: 3

leucinzip. L(6)L(6)L(6)L(6)L

12/45



Fig. 12

human : GDVEK G K KIFIMKCSQCHTVEKGG KHKTPNHLHGLFGRK ... SEQ ID NO: 1  
bacterium : E GDAAAGEKVS KCLACHTFDQGGANKV GPNPN LFGVF... SEQ ID NO: 2

**Fig. 23 A**



1	TEEQIAEFKE	AFSLFDKDG
21	GTITTKELGT	VMRSLGQNPT
41	EAE LQDMINE	VDADGNGTID
61	FPEFLTMMAR	KMKD TDSEEE
81	IREAFRVFDK	DGNGYISAAE
101	LRHVMTNLGE	KLTD EEVDEM
121	IREANIDGDG	QVNYEEFVQM
141	MTA	

AMINO ACID SEQUENCE OF CALMODULIN SEQ ID No: 4  
(EXCERPT FROM PDB)

**Fig. 23 B**

1	AMDQQA EARA	FLSEEMIAEF
21	KAAFD MF DAD	GGGDI STKEL
41	GTVMRMLGQN	PTKEELDAII
61	EEVDE DGS GT	IDFEEFLVM
81	VRQMKEDAKG	KSEEEELADCF
101	RIFDKNADGF	IDIEELGEIL
121	RATGEHVTEE	DIEDLMKDSD
141	KNNDGRIDFD	EFLKMMEGVQ
161		

AMINO ACID SEQUENCE OF TROPONIN C SEQ ID No: 5  
(EXCERPT FROM PDB)



Fig. 25

Probe site = 81-108 in Calmodulin

96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	
L	A	D	C	F	R	I	F	D	K	N	A	D	G	F	seq ID no: 6
I	R	E	A	F	R	V	F	D	K	D	G	N	G	Y	< target >
111	112	113	114	115	116	117	118	119	120	121	122	123			< probe >
I	D	I	E	E	L	G	E	I	L	R	A	T			seq ID no: 6
I	S	A	A	E	L	R	H	V	M	T	N	L			< target >
															< probe >

rmsd = 0.567034



Fig. 26

Probe site = 81-108 and 117-143 in Calmodulin

96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	seq ID no: 6
L	A	D	C	F	R	I	F	D	K	N	A	D	G	F	< target >
I	R	E	A	F	R	V	F	D	K	D	G	N	G	Y	< probe >
111	112	113	114	115	116	117	118	119	120	121	122	123			seq ID no: 7
I	D	I	E	E	E	L	G	E	I	L	R	A	T	< target >	seq ID no: 8
I	S	A	A	E	E	L	R	H	V	M	T	N	L	< probe >	seq ID no: 7
132	133	134	135	136	137	138	139	140	141	142	143	144	145		
I	E	D	L	M	K	D	S	D	K	N	N	D	G		seq ID no: 8
V	D	E	M	I	R	E	A	N	I	D	G	D	G		< target >
146	147	148	149	150	151	152	153	154	155	156	157	158			< probe >
R	I	D	F	D	E	F	L	K	M	M	E	G			seq ID no: 9
Q	V	N	Y	E	E	F	V	Q	M	M	T	A			< target >
															< probe >

rmsd = 0.823665



Fig. 29

===== ATP/GTP binding site =====

Probe = (elongation factor)

7 8 9 10 11 12 13 14  
G H V D H G K T < probe > SEQ ID NO: 10

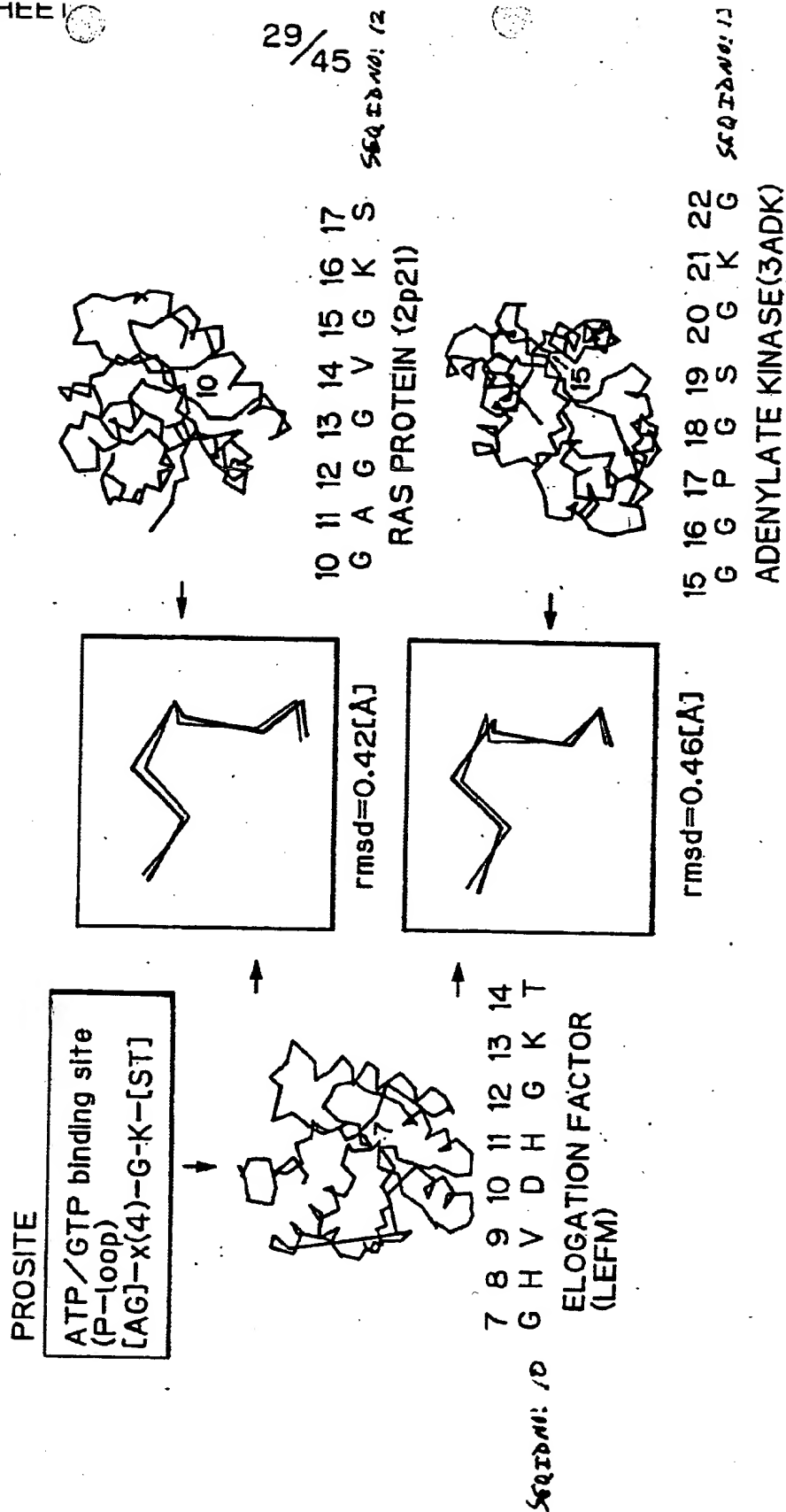
8 9 10 11 12 13 14 15  
G A P G S G K G < target >  
G H V D H G K T < probe >  
rmsd=0.648732 adenylate kinase  
SEQ ID NO: 10

unit - A

10 11 12 13 14 15 16 17  
G A G G V G K S < target > SEQ ID NO: 12  
G H V D H G K T < probe >  
rmsd=0.421770 ras protein  
SEQ ID NO: 10



Fig. 30







**Fig. 38 A**

1	I	V	G	G	Y	T	C	C	A	N	T	V	P	Y	Q	V	S	L	N	S
21	G	Y	H	F	C	G	G	S	L	I	N	S	Q	W	V	V	S	A	A	H
41	C	Y	K	S	G	I	Q	V	R	L	G	E	D	N	I	N	V	V	E	G
61	N	E	Q	F	I	S	A	S	K	S	I	V	H	P	S	Y	N	S	N	T
81	L	N	N	D	I	M	L	I	K	L	K	S	A	A	S	L	N	S	R	V
101	A	S	I	S	L	P	T	S	C	A	S	A	G	T	Q	C	L	I	S	G
121	W	G	N	T	K	S	S	G	T	S	Y	P	D	V	L	K	C	L	K	A
141	P	I	L	S	D	S	S	C	K	S	A	Y	P	G	Q	I	T	S	N	M
161	F	C	A	G	Y	L	E	G	G	K	D	S	C	Q	G	D	S	G	G	P
181	V	V	C	S	G	K	L	Q	G	I	V	S	W	G	S	G	C	A	Q	K
201	N	K	P	G	V	Y	T	K	V	C	N	Y	V	S	W	I	K	Q	T	I
221	A	S	N																	

SEQ ID NO: 14

AMINO ACID SEQUENCE OF TRYPSIN (EXCERPT FROM PDB)

**Fig. 38 B**

1	V	V	G	G	T	E	A	Q	R	N	S	W	P	S	Q	I	S	L	Q	Y
21	R	S	G	S	S	W	A	H	T	C	G	G	T	L	I	R	Q	N	W	V
41	M	T	A	A	H	C	V	D	R	E	L	T	F	R	V	V	V	G	E	H
61	N	L	N	Q	N	N	G	T	E	Q	Y	V	G	V	Q	K	I	V	V	
81	P	Y	W	N	T	D	D	V	A	A	G	Y	D	I	A	L	L	R	L	A
101	Q	S	V	T	L	N	S	Y	V	Q	L	G	V	L	P	R	A	G	T	I
121	L	A	N	S	P	C	Y	I	T	T	G	W	G	L	T	R	T	N	G	Q
141	L	A	Q	T	L	Q	Q	A	Y	L	P	T	V	D	Y	A	I	C	S	S
161	S	S	Y	W	G	S	T	V	K	N	S	M	V	C	A	G	G	D	G	V
181	R	S	G	C	Q	G	D	S	G	G	P	L	H	C	L	V	N	G	Q	Y
201	A	V	H	G	V	T	S	F	V	S	R	L	G	C	N	V	T	R	K	P
221	T	V	F	T	R	V	S	A	Y	I	S	W	I	N	N	V	I	A	S	N

SEQ ID NO: 15

AMINO ACID SEQUENCE OF ELASTASE (EXCERPT FROM PDB)



## Fig 39 A

Key site number 36 - 41 in Trypsin

41	42	43	44	45	46		
M	T	A	A	H	C	< target >	SEQ ID NO: 16
V	S	A	A	H	C	< probe >	SEQ ID NO: 17

d = 12.070038 [A]

r.m.s.d. = 0.061077 [A]

The number of atoms in a probe = 6

The number of atoms in PDB = 240

The number of combination = 1

Time = 1sec

RETRIEVED RESULTS OF HISTIDINE ACTIVE SITES

## Fig. 39 B

Key site number 175 - 179 in Trypsin

186	187	188	189	190		
G	D	S	G	G	< target >	SEQ ID NO: 18
G	D	S	G	G	< probe >	SEQ ID NO: 19

d = 8.922721 [A]

r.m.s.d. = 0.092879 [A]

The number of atoms in a probe = 5

The number of atoms in PDB = 240

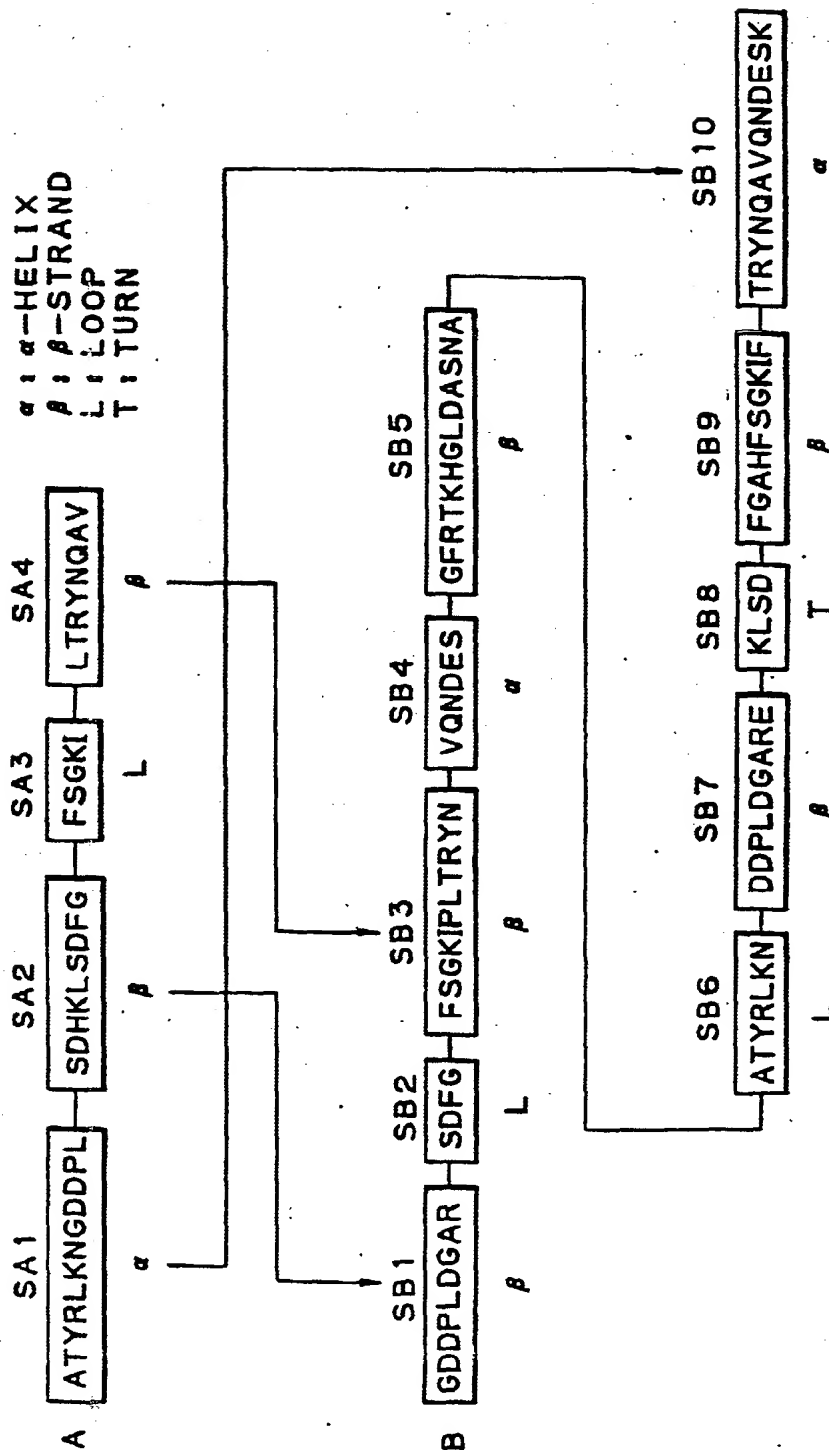
The number of combination = 1

Time = 1sec

RETRIEVED RESULTS OF SERINE ACTIVE SITES



Fig. 46



SEQ ID NO: 20